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10/087,035	02/27/2002	Robert Kincaid	1001011076-1	6480

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EXAMINER	
SMITH, CAROLYN L	
ART UNIT	PAPER NUMBER
1631	

NOTIFICATION DATE	DELIVERY MODE
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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Notice of the Office communication was sent electronically on above-indicated "Notification Date" to the following e-mail address(es):

IPOPS.LEGAL@agilent.com

Office Action Summary	Application No.	Applicant(s)	
	10/087,035	KINCAID, ROBERT	
	Examiner	Art Unit	
	Carolyn Smith	1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *26 May 2009*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-11,22,27,28,31-37,41-44 and 47-54* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-11,22,27,28,31-37,41-44 and 47-54* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Applicant's amendments and remarks, filed 5/26/09, are acknowledged. Amended claims 1, 22, 27, 52 and new claim 54 are acknowledged.

Applicant's arguments, filed 5/26/09, have been fully considered but they are not deemed to be persuasive. Rejections and/or objections not reiterated from the previous office actions are hereby withdrawn. The following rejections and/or objections are either reiterated or newly applied. They constitute the complete set presently being applied to the instant application.

Claims herein under examination are 1-11, 22, 27-28, 31-37, 41-44, and 47-54.

Claim Rejections – 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

Claims 1-11, 22, 27-28, 31-37, 41-44, and 47-54 are rejected under 35 U.S.C. 103(a) as being unpatentable over Zhou et al. (US 2003/0120432 A1) further in view of Markowitz et al. (US 2003/0100999) and Cracauer et al. (US 2007/0178474). This rejection is maintained for

claims 1-11, 22, 27-28, 31-37, 41-44, and 47-53, necessitated by amendment for claim 54, and reiterated for reasons of record.

Zhou et al. describe a method for generating a custom probe array design wherein a system receives user-selected identifiers (array design parameters) (abstract), as stated in instant claims 1, 6, 22. Zhou et al. describe the user selecting probe set identifiers from a corresponding list that corresponds to a gene (paragraphs 0009). Zhou et al. describe a user computer system (i.e. first computer) and a web portal processes inquiries regarding biological information for microarray experiments and a user selects « probe set identifiers » which enable detection of nucleic acids and corresponding genes which are identified (paragraphs 0005, 0009), a user requesting a corresponding probe set for a specified gene sequence (0093), and receiving one or more genes from a user as well as user notations (0168 and 0169) as well as accepting information from a remote user using a computer (i.e. second computer) (0082) which represents receiving from a customer, at least one array design parameter and notification of at least one gene of interest (as stated in instant claims 1, 22, 27) as well as selecting using a first computer and sending data to a second computer (as stated in instant claim 52). Zhou et al. describe accessing databases to provide researchers with associations between probe sets and gene identifiers, using Entrez search and retrieval system that provides information from various NCBI databases including nucleotide sequences (i.e. raw sequence data), including accessing NCBI Entrez nucleotide database, and associations of a gene or probe-set identifier to products and a genomics database (0075, 0076, 0084, 0033, 0027, 0028, 0034), a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed (0093), and accessing/searching a database to

obtain sequence data for probe selection for at least one gene of interest such that the correspondence may be provided to the user (0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122), searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers (0124), or analyzing user provided input sequence to determine which portions should be represented by probes (0125), and databases including information relating probe set identifiers to probe sequences (0114) which represents database searching to obtain sequence data for probe selection for at least one gene of interest comprising obtaining raw sequence data from a search based upon said at least one gene of interest, as stated in instant claims 1, 22, 27, and 50-53. Zhou et al. describe analyzing a sequence to determine which portions of the sequence should be represented by probes which does not include short, common repeats because they are ineffective in uniquely representing the sequence (0125). Zhou et al. describe the verifier/designer applies various criteria and tests to verify and selects or designs probe sequences appropriate for representing the user-provided sequence (0125, 0140), as stated in instant claims 1, 22, 27, 52, 53. Zhou et al. describe the user may select many probe array format factors such as number of probes, dimensions of probes, maximum number of probes representing one or more genes, substrate material that are received from the user (0009, 0138, 0140) which represents providing/receiving other selected array design parameters from the customer, as stated in instant claim 1. Zhou et al. describe a probe array generator that generates a custom probe array design from the associated probe sets and probe array format information (0142) and synthesizes the probe arrays (0010) which represents completing the array design and fabricating the array, as stated in instant claims 1, 22, 27, 28. Zhou et al. describe the genomic

portal system receives user-selected identifiers including sequence information, the system verifies probes corresponding to identifiers and generates a custom probe array design (paragraphs 0006 and 0008) and constructing and arranging arrays to detect and/or measure any one gene expression (paragraph 0007). Zhou et al. describe using remote vendor business systems and servers (Figure 4, #404 and paragraph 0134) and the user data processor then receiving the custom probe array design, as stated in instant claims 1, 2, 22, 27, 31. Zhou et al. describe further generation including modifying or rejecting one or more user-selected probe array format factors including user-selected probe set identifiers and displaying this information to the user (paragraph 0010) which represents the vendor selecting at least one probe specific for the gene sequence, as stated in instant claims 1, 22, 27, 52, 53. Zhou et al. describe a verifier/designer performs an analysis of the user-provided input sequence to determine which portions of the sequence should be represented by probes because some portions may consist of short, common repeats that are not effective in uniquely representing the sequence as a whole (paragraph 0125) and using masks (paragraph 0063). Zhou et al. describe analyzing the complexity of the user-provided sequence and report that the sequence is insufficiently complex with too many repeats to be uniquely and/or reliably represented by a probe set (paragraph 0126). Zhou et al. describe a method and system (vendor) enabling a number of users to share space on an array or enabling a number of users to share in ordering portions of a lot of catalog probe arrays for economical benefit (paragraphs 0005 and 0006), which represents the vendor providing at least one additional array design parameter including probe selection as well as layout parameters, as stated in instant claims 1, 5, 27, 34, 52, 53. Zhou et al. describe the user may select many probe array format factors such as number of probes, dimensions of probes,

maximum number of probes representing one or more genes, substrate material that are received from the user (paragraph 0009) which represents receiving other selected array design parameters from the customer, as stated in instant claims 33-36. Zhou et al. describe the user may select geographic dispersion of probe sets and the user may provide some or all of the array format factors, such as substrate material or design, that are received by the user (paragraph 0009) which represents array design layout and probe parameters received from the customer, as stated in instant claims 5, 6, 34, and 35. Zhou et al. describe receiving array design layout and probe parameters from the customer and using a probe set with controls (paragraphs 0009, 0074, 0090), as stated in instant claims 7 and 36. Figure 14 shows a graphical user interface for providing options and design selections (paragraph 0039), as stated in instant claims 8 and 37. Figure 15 shows a graphical user interface for providing one or more custom probe array designs or probe set designs (layouts) (paragraphs 0010 and 0040) which represents outputting at least one array design (as stated in instant claims 1, 22, 27, and 52) and visual display of array layout of at least one customer selected array design parameter (as stated in instant claim 9). Zhou et al. describe receiving probe set identifiers that identify potential probes and verifying probe sets of verified probes (paragraph 0007), which represents some probe selection by a vendor, as stated in instant claims 1, 27, 52. Zhou et al. describe displaying the custom probe array design to the user via graphical user interface and receives a user selection specifying acceptance, modification, or rejection of the design and providing accepted or modified custom probe array as well as vendor completing (i.e. shared probe array deemed complete) or customer completing (i.e. particular type of probe set ordered by user) an array design (abstract and Figure 15, 0145), as stated in instant claims 10 and 11. The user acceptance of array design represents completion

of the design by the vendor, as stated in instant claims 1, 2, 22, 27, 31, 52. The user modification of the design represents completion of the array design by the customer, as stated in instant claims 1, 3, 22, 27, 32. Zhou et al. describe providing the user with the accepted or modified custom probe array (abstract). Zhou et al. describe using arrays for genes and nucleic acids (Figure 2 #230), as stated in instant claims 4, 22, and 27. Zhou et al. describe researchers using microarrays to determine which genes are expressed in certain cells or organs, extracting biological information, and designing follow-up experiments (paragraph 0004). Zhou et al. describe the probe set identifiers may be selected by the user from a predetermined list where each item may correspond to an EST, gene, splice variant, or protein (paragraph 0009) which represents selecting at least one gene of interest and probe parameter for said gene, as stated in instant claim 27. Zhou et al. describe systems, methods, and computer program products to address these needs, such as allowing the user to select probe identifiers that may be associated with probe sets of one or more probes that are capable of detecting genes of interest, which are then correlated with data and/or products to be provided to the user (paragraph 0006), as stated in instant claim 27. Figures 7A and 10 show displaying and providing genomic data, sequence data, expression data, and various other forms of information to the user (paragraphs 0030 and 0034), as stated in instant claim 27. Zhou et al. describe synthesizing probes on a substrate (paragraph 0090), as stated in instant claim 28. Zhou et al. describe selecting substrate material or design and synthesized probe arrays (paragraph 0010), as stated in instant claim 28. Zhou et al. describe constructing probe arrays to detect or measure one or any combination of biological information including gene expression, genotype, cells, cellular membranes, and organelles (paragraph 0007) which represents an in situ array, as stated in instant claim 41. Zhou et al.

describe users may formulate queries to obtain BLAST similarity searches (0078), which represents searching using the BLAST search algorithm, as stated in instant claim 54. Zhou et al. provisional (60/301,298) does not specifically state curating or curated sequence (instant claim 1, steps c) and d), 52, 53) or describe all of the curating limitations in claims 42-44 and 47-49.

Markowitz et al. describe offering gene chip technology manufacturing glass microarrays with probes (0006). Markowitz et al. describe using custom gene sequences (0037), user selection and user-selected gene attributes (parameters) (0110, 0229) allowing users to specify parameters and adjust parameters (0050), sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets (0249), BLAST searching (0045), and sequence based matching and manual data curation including detecting potential sequence data contamination (0043, 0046) which represents database searching and curating sequence data, as stated in instant claims 1, 22, 27, 52. Markowitz et al. describe the user entering search parameters with the search completing by listing Affy fragments that match the input sequence (0253) and the Gene Set Import Utility allowing a user to create a Gene Set based on a list of Affy probe set names wherein the user-selected return attribute values are queried followed by displaying the query results after which the user can save the fragments if he/she wishes (0255, 0245) which represents completing the array design by the customer, as stated in instant claim 3. Markowitz et al. do not describe all of the curating limitations in claims 42-44 and 47-49.

Cracauer et al. describe a high-throughput oligonucleotide production system (claim 1), a computer system of a customer (i.e. first computer) communicatively linked to a remote vendor

processor (i.e. second computer) (0023, 0031, 1053-1057), designing and producing detection assays for target sequences (0434), and receiving orders from a customer who enters a target sequence into a web interface, processing orders, obtaining raw data from the web order entry component and designing the detection assays which can be produced and shipped to customers (0435, 0539, 1056-1069). Cracauer et al. describe searching databases to obtain sequence data, identifying problems where the system can automatically remove problem portions of the sequence such as repeat or artifact sequences (i.e. stored programming for curation) (0318, 0502-0504), searching nucleic acid databases including BLAST (0071, 0447, 0453, 0460, 0477-0478), a curated sequence (0484), and checking for errors in target sequence and removal of artifacts associated with sequence assembly and removal of commonly repeated subsequences (0443-0444, 0467-0475, 0541, 0101, 0369, 0503-0505, 0653) as stated in instant claims 42-44, 47-49, and 52-53.

Zhou et al. state researchers are increasingly challenged to extract biologically meaningful information from the vast amounts of data generated by microarray technologies and to design follow-up experiments (0004). Cracauer et al. state attempts to analyze individuals based on a reference genome sequence will often fail (i.e. probes based on reference sequence fail to hybridize to target sequence in another individual) because the target sequence for many individuals differs from the reference sequence (0022). It would have been obvious to one of ordinary skill in the art at the time the invention was made to modify the method of Zhou et al. by sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets as taught by Markowitz et al. wherein the motivation would have been to provide a common interface for multiple databases in

a relational format to support efficient exploration and analysis, as stated by Markowitz et al. (0009) in order to extract meaningful information, as stated by Zhou et al. (0004). It would have been further obvious to one of ordinary skill in the art at the time the invention was made to modify the methods of Zhou et al. and Markowitz et al. by checking for errors and removal of sequence artifacts as taught by Cracauer et al. where the motivation would have been to select appropriate target sequences that can be successfully targeted by detection assays (0442) in order to extract meaningful information (Zhou et al. 0004).

Thus, Zhou et al. in view of Markowitz et al. and Cracauer et al. make obvious the instant invention.

Applicant states the Examiner admitted 60/301298 does not disclose curating as claimed. It is noted that Zhou et al. provisional (60/301,298) does not specifically state curating or curated sequence (instant claim 1, steps c) and d), 52, 53) or describe all of the curating limitations in claims 42-44 and 47-49. It is further noted that this is a 35 USC 103 rejection such that not all limitations need to come from a single reference. Applicant admits they did not invent curating in general. Applicant argues Markowitz et al. teaches away from curating sequences by computer using software configured for this task because Markowitz et al. describe manual data curation. This statement is found unpersuasive as performing something manually does not teach away from a limitation. Automating a manual activity does not distinguish over prior art and does not teach away from the limitation.

As stated in MPEP 2144.04:

In re Venner, 262 F.2d 91, 95, 120 USPQ 193, 194 (CCPA 1958) (Appellant argued that claims to a permanent mold casting apparatus for molding trunk pistons were allowable over the prior art because the claimed invention combined "old permanent-mold structures together with a timer and solenoid which automatically actuates the known pressure valve system to release the inner core after a predetermined time has elapsed." The court held that broadly providing an automatic or mechanical means to replace a manual activity which accomplished the same result is not sufficient to distinguish over the prior art.)

Applicant argues that Cracauer et al. fail to teach curation is performed using stored programming for sequence curation by a computer system configured for curation of sequences. This statement is found unpersuasive as Cracauer et al. describe searching databases to obtain sequence data, identifying problems where the system can automatically remove problem portions of the sequence such as repeat or artifact sequences (i.e. stored programming for curation) (0318, 0502-0504), searching nucleic acid databases (0071, 0447, 0453, 0460, 0477), a curated sequence (0484), and checking for errors in target sequence and removal of artifacts associated with sequence assembly and removal of commonly repeated subsequences (0443-0444, 0467-0475, 0541, 0101, 0369, 0503-0505, 0653).

Applicant argues that Zhou et al. teach away from modifications because 60/301298 specifically discloses that the system does not include blasting capabilities when a search is performed on page 7, under "2.3.2 Constraints". This statement is found unpersuasive as the following section "2.3.3 Dependencies" on page 7 states: "The Portal project will provide the sequence blasting capabilities the Flexible Content needs". Page 13 states "this page will integrate with the Portal to allow users to search by blasting sequences also." In addition, Markowitz et al. (0045) and Cracauer et al. (0478) both use BLAST, a well known search

algorithm. Applicant argues Markowitz et al. has nothing to do with design or fabrication of arrays. This statement is found unpersuasive as Markowitz et al. describe the following:

Markowitz et al. describe offering gene chip technology manufacturing glass microarrays with probes (0006). Markowitz et al. describe using custom gene sequences (0037), user selection and user-selected gene attributes (parameters) (0110, 0229) allowing users to specify parameters and adjust parameters (0050), sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets (0249), and sequence based matching and manual data curation including detecting potential sequence data contamination (0043, 0046) which represents database searching and curating sequence data, as stated in instant claims 1, 22, 27, 52. Markowitz et al. describe the user entering search parameters with the search completing by listing Affy fragments that match the input sequence (0253) and the Gene Set Import Utility allowing a user to create a Gene Set based on a list of Affy probe set names wherein the user-selected return attribute values are queried followed by displaying the query results after which the user can save the fragments if he/she wishes (0255, 0245) which represents completing the array design by the customer, as stated in instant claim 3.

Applicant reiterates that they did not invent the broad concept of curation. Applicant argues that Markowitz et al. has nothing to do with selection of probes or array design as claimed. It is noted that gene chip technology manufacturing arrays with probes with custom genes and user selected gene attributes, etc. which does involve probes and array design. Applicant argues the present claims recite selecting at least one gene of interest, and argues Zhou et al. do not describe notification of at least one gene of interest received from a customer. It is noted that Zhou et al. specifically states in paragraph 0169 that the method receives gene information from a user. Receiving gene information encompasses receiving notification of at least one gene of interest.

Applicant argues there has to be reason to combine references. It is noted that a motivation to combine references has been stated (see end of 35 USC 103 rejection). It is further noted that the motivation for combining references need not be for the same motivations as

Applicant. The fact that applicant has recognized another advantage which would flow naturally from following the suggestion of the prior art cannot be the basis for patentability when the differences would otherwise be obvious. See *Ex parte Obiaya*, 227 USPQ 58, 60 (Bd. Pat. App. & Inter. 1985).

Applicant argues that Zhou et al. teach away from performing a database search of the type recited in the present claims. This statement is found unpersuasive as it is conclusory. Zhou et al. describe users may formulate queries to obtain BLAST similarity searches (0078), which represents searching using the BLAST search algorithm. In addition, Markowitz et al. (0045) and Cracauer et al. (0478) both use BLAST, a well known search algorithm.

Applicant argues paragraphs 0093, 0124, and 0125 of Zhou et al. are not in the provisional 60/301298. This statement is found unpersuasive as the limitations relied upon are present in 60/301298. 0093 of Zhou et al. state a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed. Such limitations can be found on pages 1 and 18 of 60/301298. 0124 of Zhou et al. states searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers. Such limitations can be found on pages 8 and 16-18 of 60/301298. 0125 of Zhou et al. states analyzing user provided input sequence to determine which portions should be represented by probes. Such limitations can be found on pages 4 and 8-9 of 60/301298.

Applicant summarizes part of the 35 USC 103 rejection, argues that instant claims do not recite a user selecting probe set identifiers from a corresponding list that corresponds to a gene",

but rather recite at least one gene of interest, having been selected by a customer, that is received from a customer. This statement is found unpersuasive as Zhou et al. describe a web portal processes inquiries regarding biological information for microarray experiments and a user selects « probe set identifiers » which enable detection of nucleic acids and corresponding genes which are identified (paragraphs 0005, 0009), as user requesting a corresponding probe set for a specified gene sequence (0093), and receiving one or more genes from a user as well as user notations (0168 and 0169) which represents receiving from a customer, at least one array design parameter and notification of at least one gene of interest. Indeed, Zhou et al. specifically states in paragraph 0169 that the method receives gene information from a user. Applicant argues that the claimed method has the capability of obtaining sequence data from which to select probes which is not within the capability of the cited references. This statement is found unpersuasive as sequence data is obtained in Zhou et al. as described below:

Zhou et al. describe accessing databases to provide researchers with associations between probe sets and gene identifiers, using Entrez search and retrieval system that provides information from various NCBI databases including nucleotide sequences (i.e. raw sequence data), including accessing NCBI Entrez nucleotide database, and associations of a gene or probe-set identifier to products and a genomics database (0075, 0076, 0084, 0033, 0027, 0028, 0034), a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed (0093), and accessing/searching a database to obtain sequence data for probe selection for at least one gene of interest such that the correspondence may be provided to the user (0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122), searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers (0124), or analyzing user provided input sequence to determine which portions should be represented by probes (0125), and databases including information relating probe set identifiers to probe sequences (0114) which represents database searching to obtain sequence data for probe selection for at least one gene of interest comprising obtaining raw sequence data from a search based upon said at least one gene of interest.

Applicant argues paragraph 0009 of Zhou et al. is not in the provisional 60/301298. This statement is found unpersuasive as the limitations relied upon are present in 60/301298. 0009 states the user selecting probe set identifiers from a corresponding list that corresponds to a gene. Such limitations are found on page 4, 8-9, and 18-19 of 60/301298. Applicant argues that none of the information from Zhou et al.'s paragraphs 0093, 0168, and 0169 are in provisional application 60/301,298. This statement is found unpersuasive as 60/301298 describes custom design based on sequences provided by a customer (page 2) and a requestor completing a FCA (flexible content array design) (page 5). In addition, Markowitz et al. describe using custom gene sequences (0037), user selection and user-selected gene attributes (parameters) (0110, 0229) allowing users to specify parameters and adjust parameters (0050), sequence searching for a user-provided nucleotide sequence against a database of GenBank sequences corresponding to Affymetrix (vendor) probe sets (0249), and sequence based matching and manual data curation including detecting potential sequence data contamination (0043, 0046). Cracauer et al. describe a high-throughput olignucleotide production system (claim 1), designing and producing detection assays for target sequences (0434), and receiving orders from a customer who enters a target sequence into a web interface, processing orders, and designing the detection assays which can be produced and shipped to customers (0435, 0539). Applicant reiterates some arguments that have already been found unpersuasive for reasons given above.

Applicant summarizes Zhou et al's paragraphs 0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122 and argues these passages do not describe accessing/searching a database to obtain data for probe selection for at least one gene of interest such that correspondence may be provided to the user. This statement is found unpersuasive as Zhou et al. describe these

limitations given their broad and reasonable interpretations (i.e. sequence data can be any data related to a sequence). Zhou et al. describe gene accession numbers with correspondence between probe sets and genes maintained in a database and obtaining genomic data related to a selected accession number which is provided to a user (0095). In addition, Zhou et al. describe accessing databases to provide researchers with associations between probe sets and gene identifiers, using Entrez search and retrieval system that provides information from various NCBI databases including nucleotide sequences, including accessing NCBI Entrez nucleotide database, and associations of a gene or probe-set identifier to products and a genomics database (0075, 0076, 0084, 0033, 0027, 0028, 0034), a user requesting a corresponding probe set for a specified gene sequence, and a database with the sequence or sequences from which the probes are designed (0093), and accessing/searching a database to obtain sequence data for probe selection for at least one gene of interest such that the correspondence may be provided to the user (0095, 0096, 0124, 0110, 0112, 0116, 0119, 0122), searching database for user provided sequence to verify existence of one or more corresponding probe sets and correlating identity of probe sets having a corresponding sequence with probe set identifiers (0124), or analyzing user provided input sequence to determine which portions should be represented by probes (0125), and databases including information relating probe set identifiers to probe sequences (0114) which represents database searching to obtain sequence data for probe selection for at least one gene of interest. Applicant argues the accessing/searching a database is not present in provisional 60/301298. This statement is found unpersuasive as 60/301298 recites various databases (pages 2 and 3), sequence blasting (Section 2.3.3), and search query (page 8, last paragraph).

Applicant summarizes Cracauer et al. and argues it is not prior art. This statement is found unpersuasive since it describes at least one of the rejected limitations. Applicant reiterates arguments that have already been found unpersuasive.

Applicant states he does not understand why pdf copies of the provisional applications cannot be sent with the office actions. It is noted that Applicant has already acknowledged that he has copies of the provisional applications (i.e. Applicant mailed copies of 60/301298 and 60/265103 to the USPTO on 2/28/07), making this point moot. Applicant requests Examiner to specifically point out where, in each priority documents, relied upon for Zhou et al. and Cracauer et al. the support for arguments exist. It is noted that the Examiner has provided sufficient evidence of the obviousness ground of rejection.

As stated in the previous two office actions, it is noted that the declaration filed by Applicant on 1/21/05 states the invention was conceived prior to July 16, 2001. Zhou et al.'s provisional 60/301298 was filed June 25, 2001. The Examiner wonders if Applicant can and is willing to swear behind the date of 60/301298 (which is less than a month earlier than what has already been sworn behind).

Conclusion

No claim is allowed.

Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Papers related to this application may be submitted to Technical Center 1600 by facsimile transmission. Papers should be faxed to Technical Center 1600 via the PTO Fax Center. The faxing of such papers must conform with the notices published in the Official Gazette, 1096 OG 30 (November 15, 1988), 1156 OG 61 (November 16, 1993), and 1157 OG 94 (December 28, 1993) (See 37 CFR §1.6(d)). The Central Fax Center number for official correspondence is (571) 273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. If you have questions on access to the Private PAIR

system, please contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, please call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Carolyn Smith, whose telephone number is (571) 272-0721. The examiner can normally be reached Monday through Thursday from 8 A.M. to 6:30 P.M.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie Moran, can be reached on (571) 272-0720.

August 6, 2009

/Carolyn Smith/
Primary Examiner
AU 1631